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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/024,370

DATE: 04/12/2002

TIME: 14:26:43

Input Set : A:\21123139.app

Output Set: N:\CRF3\04122002\J024370.raw

3 <110> APPLICANT: TILG, YVONNE  
 4 ELKMANN, BERND  
 5 EGGELING, LOTHAR  
 6 SAHM, HERMANN  
 7 MOCKEL, BETTINA  
 9 <120> TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF L-AMINO ACIDS BY  
 10 FERMENTATION AND NUCLEOTIDE SEQUENCES CODING FOR THE  
 11 accDA GENE  
 13 <130> FILE REFERENCE: 21123-284139-MAS  
 15 <140> CURRENT APPLICATION NUMBER: 10/024,370  
 16 <141> CURRENT FILING DATE: 2001-12-21  
 18 <150> PRIOR APPLICATION NUMBER: 09/362,899  
 19 <151> PRIOR FILING DATE: 1999-07-29  
 21 <150> PRIOR APPLICATION NUMBER: DE 199 24 365.4  
 22 <151> PRIOR FILING DATE: 1999-07-29  
 24 <160> NUMBER OF SEQ ID NOS: 3  
 26 <170> SOFTWARE: PatentIn Ver. 2.1  
 28 <210> SEQ ID NO: 1  
 29 <211> LENGTH: 2123  
 30 <212> TYPE: DNA  
 31 <213> ORGANISM: Corynebacterium glutamicum  
 33 <220> FEATURE:  
 34 <221> NAME/KEY: gene  
 35 <222> LOCATION: (508)..(1980)  
 36 <223> OTHER INFORMATION: accDA  
 38 <400> SEQUENCE: 1  
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 40 cttatatgtt tctcaccaca tctggccgac gaccacgaag tatgttgtcg atcacagcta 120  
 41 aacgtgtgaa tgtgaagtta cctaactcac attgcaatgc gatagcgatt tggaaaactc 180  
 42 actcccccca atatcttaac ttaaacttaa aagtagtggt ttacctgcat ttataaaagt 240  
 43 tcccgatcta cccctctttt accccgaaat accccttttg caaagattgc aaacacaaca 300  
 44 gtgcaatagt taacgggctt cacacgtcac cattctgtcc ggttttaggc tatgttcggg 360  
 45 acgtctaggc aaaaagtagt tttgtgagat gaaacgcata atccgtcatt ttttacgcaa 420  
 46 tcgatagcct aaattgggct tagatcttcc gcctctaaat aggtatgcag agacattoga 480  
 47 attaatgaac aaagccattt ttcggccggtg gagaagcgtt ttccgactat ggtgtggggc 540  
 48 atggaacaca cttcagcatt gacgctcata gactcgggtt tggaccctga cagcttcatt 600  
 49 tcttggaatg aaactcccca atatgacaac ctcaatcaag gctatgcaga gaccttggag 660  
 50 cgggctcgaa gcaaggccaa atgcgatgaa tcggtaatta ctggagaagg caccgtggag 720  
 51 ggcattccgg tagccgttat tttgtccgat ttttcttcc tcggcggttc tttgggcacg 780  
 52 gtcgcgctcg tgccgcatcat gaaggcgatt caccgcgcca cagagctgaa actccactcg 840  
 53 ctggtctccc ctgcttccgg tgggtgcgcgc atgcaggaag acaatcgagc ttttgtcatg 900  
 54 atggtgtcca taaccgcggc tgtgcagcgt caccgcgagg cgcatttgcc gttcctggtg 960  
 55 tatttgcgca atcccacgat ggggtggcgcc atggcctcgt ggggttcacg tgggcatctc 1020

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56 acttttgcgg aaccgcggcg gcagataggt ttcctgggtc ctgcgctggt ggagttaacc 1080
57 actgggcatg cgcttccaga cgggtgtgcag caggcggaga atttggtgaa aactggtgtg 1140
58 attgatggaa ttgtgtcgcc actccaattg cgtgcagcgg tggcaaaaac cctcaagggt 1200
59 attcagccgg tagaggcaac ggatcgtttt tctccaacaa ctccctggcg ggcaattccg 1260
60 gtgatggagg cgattgcgcy ttctcgtgac ccgcagaggg ctggaatcgg ggagattatg 1320
61 gaaacgttgg gggcagacgt cgtcaagctt tctggtgcgc gtgctggcgc attgagcccg 1380
62 gctgtgcgcy ttgccctggc gcgcacgcgg ggccggcccg tgggtgctgat tgggcaggat 1440
63 cgccgcttca cgcttggggc gcaggagctg cgttttgcgc gtcgtggcat ttcgctggcg 1500
64 cgcgagctaa acctgccgat cgtgtccatc atcgacacct ccggcgccga attgtgcgag 1560
65 gcggctgagg agctcggcat cgcaagctcg attgcgcgca ccttgtccaa gcttatcgac 1620
66 gctcccctcc ccaccgtttc ggtcattatt ggtcagggcg ttggcggtgg cgcgctggcc 1680
67 atgctgcccg ccgatctggt ctacgcggcc gaaaacgcgt ggctgtccgc attgccacca 1740
68 gagggcgccct cggccatcct cttccgcgac accaaccacg ccgcggaaat catagagcga 1800
69 caaggcgtgc aggcgcacgc acttttaagc caagggttta tcgacgggat cgtcgccgaa 1860
70 accgagcact ttgttgaaga aattctcgcc acaatcagca acgccccttc cgaattggat 1920
71 aacaatccgg agagggcggg acgcgacagt cgcttcacac gatttgagcg tttagcgcag 1980
72 taaagaaaat tatgcgctga tcaaatcgat gatgaacacc agggtagcgc cagacagtgg 2040
73 gtggccggaa ccctcagggc cgtaagcagc ctctggcgga atggtcagct gacgacgtcc 2100
74 gccgaccttc atgcctggaa ttc                                     2123

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77 &lt;210&gt; SEQ ID NO: 2

78 &lt;211&gt; LENGTH: 1473

79 &lt;212&gt; TYPE: DNA

80 &lt;213&gt; ORGANISM: Corynebacterium glutamicum

82 &lt;220&gt; FEATURE:

83 &lt;221&gt; NAME/KEY: CDS

84 &lt;222&gt; LOCATION: (1)..(1473)

85 &lt;223&gt; OTHER INFORMATION: accDA

87 &lt;400&gt; SEQUENCE: 2

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88 gtg gag aag cgt ttt ccg act atg gtg tgg ggc atg gaa cac act tca 48
89 Val Glu Lys Arg Phe Pro Thr Met Val Trp Gly Met Glu His Thr Ser
90 1 5 10 15
92 gca ttg acg ctc ata gac tcg gtt ttg gac cct gac agc ttc att tct 96
93 Ala Leu Thr Leu Ile Asp Ser Val Leu Asp Pro Asp Ser Phe Ile Ser
94 20 25 30
96 tgg aat gaa act ccc caa tat gac aac ctc aat caa ggc tat gca gag 144
97 Trp Asn Glu Thr Pro Gln Tyr Asp Asn Leu Asn Gln Gly Tyr Ala Glu
98 35 40 45
100 acc ttg gag cgg gct cga agc aag gcc aaa tgc gat gaa tcg gta att 192
101 Thr Leu Glu Arg Ala Arg Ser Lys Ala Lys Cys Asp Glu Ser Val Ile
102 50 55 60
104 act gga gaa ggc acc gtg gag ggc att ccg gta gcc gtt att ttg tcc 240
105 Thr Gly Glu Gly Thr Val Glu Gly Ile Pro Val Ala Val Ile Leu Ser
106 65 70 75 80
108 gat ttt tcc ttc ctc ggc ggt tct ttg ggc acg gtc gcg tcg gtg cgc 288
109 Asp Phe Ser Phe Leu Gly Gly Ser Leu Gly Thr Val Ala Ser Val Arg
110 85 90 95
112 atc atg aag gcg att cac cgc gcc aca gag ctg aaa ctc cca ctg ctg 336
113 Ile Met Lys Ala Ile His Arg Ala Thr Glu Leu Lys Leu Pro Leu Leu
114 100 105 110

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116 gtc tcc cct gct tcc ggt ggt gcg cgc atg cag gaa gac aat cga gct 384
117 Val Ser Pro Ala Ser Gly Gly Ala Arg Met Gln Glu Asp Asn Arg Ala
118      115      120      125
120 ttt gtc atg atg gtg tcc ata acc gcg gct gtg cag cgt cac cgc gag 432
121 Phe Val Met Met Val Ser Ile Thr Ala Ala Val Gln Arg His Arg Glu
122      130      135      140
124 gcg cat ttg ccg ttc ctg gtg tat ttg cgc aat ccc acg atg ggt ggc 480
125 Ala His Leu Pro Phe Leu Val Tyr Leu Arg Asn Pro Thr Met Gly Gly
126 145      150      155      160
128 gcc atg gcc tcg tgg ggt tca tct ggg cat ctc act ttt gcg gaa ccc 528
129 Ala Met Ala Ser Trp Gly Ser Ser Gly His Leu Thr Phe Ala Glu Pro
130      165      170      175
132 ggc gcg cag ata ggt ttc ctg ggt cct cgc gtg gtg gag tta acc act 576
133 Gly Ala Gln Ile Gly Phe Leu Gly Pro Arg Val Val Glu Leu Thr Thr
134      180      185      190
136 ggg cat gcg ctt cca gac ggt gtg cag cag gcg gag aat ttg gtg aaa 624
137 Gly His Ala Leu Pro Asp Gly Val Gln Gln Ala Glu Asn Leu Val Lys
138      195      200      205
140 act ggt gtg att gat gga att gtg tcg cca ctc caa ttg cgt gca gcg 672
141 Thr Gly Val Ile Asp Gly Ile Val Ser Pro Leu Gln Leu Arg Ala Ala
142      210      215      220
144 gtg gca aaa acc ctc aag gtt att cag ccg gta gag gca acg gat cgt 720
145 Val Ala Lys Thr Leu Lys Val Ile Gln Pro Val Glu Ala Thr Asp Arg
146 225      230      235      240
148 ttt tct cca aca act cct ggc gtg gca ctt ccg gtg atg gag gcg att 768
149 Phe Ser Pro Thr Thr Pro Gly Val Ala Leu Pro Val Met Glu Ala Ile
150      245      250      255
152 gcg cgt tct cgt gac ccg cag agg cct gga atc ggg gag att atg gaa 816
153 Ala Arg Ser Arg Asp Pro Gln Arg Pro Gly Ile Gly Glu Ile Met Glu
154      260      265      270
156 acg ttg ggg gca gac gtc gtc aag ctt tct ggt gcg cgt gct ggc gca 864
157 Thr Leu Gly Ala Asp Val Val Lys Leu Ser Gly Ala Arg Ala Gly Ala
158      275      280      285
160 ttg agc ccg gct gtg cgc gtt gcc ctg gcg cgc atc ggg ggc cgg ccc 912
161 Leu Ser Pro Ala Val Arg Val Ala Leu Ala Arg Ile Gly Gly Arg Pro
162      290      295      300
164 gtg gtg ctg att ggg cag gat cgc cgc ttc acg ctt ggg ccg cag gag 960
165 Val Val Leu Ile Gly Gln Asp Arg Arg Phe Thr Leu Gly Pro Gln Glu
166 305      310      315      320
168 ctg cgt ttt gcg cgt cgt ggc att tcg ctg gcg cgc gag cta aac ctg 1008
169 Leu Arg Phe Ala Arg Arg Gly Ile Ser Leu Ala Arg Glu Leu Asn Leu
170      325      330      335
172 ccg atc gtg tcc atc atc gac acc tcc ggc gcc gaa ttg tcg cag gcg 1056
173 Pro Ile Val Ser Ile Ile Asp Thr Ser Gly Ala Glu Leu Ser Gln Ala
174      340      345      350
176 gct gag gag ctc ggc atc gca agc tcg att gcg cgc acc ttg tcc aag 1104
177 Ala Glu Glu Leu Gly Ile Ala Ser Ser Ile Ala Arg Thr Leu Ser Lys
178      355      360      365
180 ctt atc gac gct ccc ctc ccc acc gtt tcg gtc att att ggt cag ggc 1152

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181 Leu Ile Asp Ala Pro Leu Pro Thr Val Ser Val Ile Ile Gly Gln Gly
182      370      375      380
184 gtt ggc ggt ggc gcg ctg gcc atg ctg ccc gcc gat ctg gtc tac gcg 1200
185 Val Gly Gly Gly Ala Leu Ala Met Leu Pro Ala Asp Leu Val Tyr Ala
186 385      390      395      400
188 gcc gaa aac gcg tgg ctg tcc gca ttg cca cca gag ggc gcc tcg gcc 1248
189 Ala Glu Asn Ala Trp Leu Ser Ala Leu Pro Glu Gly Ala Ser Ala
190      405      410      415
192 atc ctc ttc cgc gac acc aac cac gcc gcg gaa atc ata gag cga caa 1296
193 Ile Leu Phe Arg Asp Thr Asn His Ala Ala Glu Ile Ile Glu Arg Gln
194      420      425      430
196 ggc gtg cag gcg cac gca ctt tta agc caa ggg ctt atc gac ggg atc 1344
197 Gly Val Gln Ala His Ala Leu Leu Ser Gln Gly Leu Ile Asp Gly Ile
198      435      440      445
200 gtc gcc gaa acc gag cac ttt gtt gaa gaa att ctc ggc aca atc agc 1392
201 Val Ala Glu Thr Glu His Phe Val Glu Glu Ile Leu Gly Thr Ile Ser
202      450      455      460
204 aac gcc ctc tcc gaa ttg gat aac aat ccg gag agg gcg gga cgc gac 1440
205 Asn Ala Leu Ser Glu Leu Asp Asn Asn Pro Glu Arg Ala Gly Arg Asp
206 465      470      475      480
208 agt cgc ttc aca cga ttt gag cgt tta gcg cag 1473
209 Ser Arg Phe Thr Arg Phe Glu Arg Leu Ala Gln
210      485      490
213 <210> SEQ ID NO: 3
214 <211> LENGTH: 491
215 <212> TYPE: PRT
216 <213> ORGANISM: Corynebacterium glutamicum
218 <400> SEQUENCE: 3
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222 Ala Leu Thr Leu Ile Asp Ser Val Leu Asp Pro Asp Ser Phe Ile Ser
223      20      25      30
225 Trp Asn Glu Thr Pro Gln Tyr Asp Asn Leu Asn Gln Gly Tyr Ala Glu
226      35      40      45
228 Thr Leu Glu Arg Ala Arg Ser Lys Ala Lys Cys Asp Glu Ser Val Ile
229      50      55      60
231 Thr Gly Glu Gly Thr Val Glu Gly Ile Pro Val Ala Val Ile Leu Ser
232 65      70      75      80
234 Asp Phe Ser Phe Leu Gly Gly Ser Leu Gly Thr Val Ala Ser Val Arg
235      85      90      95
237 Ile Met Lys Ala Ile His Arg Ala Thr Glu Leu Lys Leu Pro Leu Leu
238      100      105      110
240 Val Ser Pro Ala Ser Gly Gly Ala Arg Met Gln Glu Asp Asn Arg Ala
241      115      120      125
243 Phe Val Met Met Val Ser Ile Thr Ala Ala Val Gln Arg His Arg Glu
244      130      135      140
246 Ala His Leu Pro Phe Leu Val Tyr Leu Arg Asn Pro Thr Met Gly Gly
247 145      150      155      160
249 Ala Met Ala Ser Trp Gly Ser Ser Gly His Leu Thr Phe Ala Glu Pro

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250		165		170		175
252	Gly Ala Gln Ile	Gly Phe Leu Gly	Pro Arg Val Val	Glu Leu Thr Thr		
253		180		185		190
255	Gly His Ala Leu	Pro Asp Gly Val	Gln Gln Ala Glu	Asn Leu Val Lys		
256		195		200		205
258	Thr Gly Val Ile	Asp Gly Ile Val	Ser Pro Leu Gln	Leu Arg Ala Ala		
259		210		215		220
261	Val Ala Lys Thr	Leu Lys Val Ile	Gln Pro Val Glu	Ala Thr Asp Arg		
262	225		230		235	240
264	Phe Ser Pro Thr	Thr Pro Gly Val	Ala Leu Pro Val	Met Glu Ala Ile		
265		245		250		255
267	Ala Arg Ser Arg	Asp Pro Gln Arg	Pro Gly Ile Gly	Glu Ile Met Glu		
268		260		265		270
270	Thr Leu Gly Ala	Asp Val Val Lys	Leu Ser Gly Ala	Arg Ala Gly Ala		
271		275		280		285
273	Leu Ser Pro Ala	Val Arg Val Ala	Leu Ala Arg Ile	Gly Gly Arg Pro		
274		290		295		300
276	Val Val Leu Ile	Gly Gln Asp Arg	Arg Phe Thr Leu	Gly Pro Gln Glu		
277	305		310		315	320
279	Leu Arg Phe Ala	Arg Arg Gly Ile	Ser Leu Ala Arg	Glu Leu Asn Leu		
280		325		330		335
282	Pro Ile Val Ser	Ile Ile Asp Thr	Ser Gly Ala Glu	Leu Ser Gln Ala		
283		340		345		350
285	Ala Glu Glu Leu	Gly Ile Ala Ser	Ile Ala Arg Thr	Leu Ser Lys		
286		355		360		365
288	Leu Ile Asp Ala	Pro Leu Pro Thr	Val Ser Val Ile	Ile Gly Gln Gly		
289		370		375		380
291	Val Gly Gly Gly	Ala Leu Ala Met	Leu Pro Ala Asp	Leu Val Tyr Ala		
292	385		390		395	400
294	Ala Glu Asn Ala	Trp Leu Ser Ala	Leu Pro Pro Glu	Gly Ala Ser Ala		
295		405		410		415
297	Ile Leu Phe Arg	Asp Thr Asn His	Ala Ala Glu Ile	Ile Glu Arg Gln		
298		420		425		430
300	Gly Val Gln Ala	His Ala Leu Leu	Ser Gln Gly Leu	Ile Asp Gly Ile		
301		435		440		445
303	Val Ala Glu Thr	Glu His Phe Val	Glu Glu Ile Leu	Gly Thr Ile Ser		
304		450		455		460
306	Asn Ala Leu Ser	Glu Leu Asp Asn	Asn Pro Glu Arg	Ala Gly Arg Asp		
307	465		470		475	480
309	Ser Arg Phe Thr	Arg Phe Glu Arg	Leu Ala Gln			
310		485		490		

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